

STIC Biotechnology Systems Branch

**RAW SEQUENCE LISTING
ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 1015224366
Source: PCT
Date Processed by STIC: 2/7/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

BEST AVAILABLE COPY

Raw Sequence Listing Error Summary

ERROR DETECTED
SUGGESTED CORRECTION
SERIAL NUMBER:

101522,366

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleics Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3 Misaligned Amino Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4 Non-ASCII The submitted file was **not saved** in ASCII(DOS) text, as **required** by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. **Per Sequence Rules**, each n or Xaa can only represent a single residue. Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

9 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 Invalid <213> Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

11 Use of <220> Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 PatentIn 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



PC

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/522,366

DATE: 02/07/2006
TIME: 12:49:02

Input Set : A:\Sequence_Listing_10522366.txt
Output Set: N:\CRF4\02012006\J522366.raw

3 <110> APPLICANT: National Institute of Advanced Industrial Science and Technology
5 <120> TITLE OF INVENTION: Lethal gene markers for transformant selection
7 <130> FILE REFERENCE: 332-01229
-> 9 <140> CURRENT APPLICATION NUMBER: US/10/522,366
-> 10 <141> CURRENT FILING DATE: 2005-01-25
12 <160> NUMBER OF SEQ ID NOS: 24
14 <170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply
Corrected Diskette Needed

(Pg. 1-2) ↗

STORED SEQUENCES

435 <210> SEQ ID NO: 20
436 <211> LENGTH: 330
437 <212> TYPE: DNA
438 <213> ORGANISM: E.coli
E-> 440 <400> SEQUENCE: 1-20
441 ggccgcctcg gcccgttagtag tagaaagggtt ttaaagatta cgggcattat tatcatccag 60
442 ctccgaaaac tgagaatatt aaagggtttt gtatcttaa gcctggata ccaaaaacac 120
443 caaagcagaa tgggtgggaa aaacgcgaac gctggacttg agataaaagggtt cgtaagattt 180
444 atgagtggga ttctcagcat ggtgagctt aggggtatcg tgccagtgtat ggtcagcatc 240
445 ttggctcatt tgaccctaaa acaggcaatc agttgaaagg tccagatccg aaacgaaata 300
446 tcaagaaata tctttgaggc catagcggcc 330

What is the source of genetic material?

449 <210> SEQ ID NO: 21
450 <211> LENGTH: 60
451 <212> TYPE: DNA
452 <213> ORGANISM: Artificial Sequence
454 <220> FEATURE:
E-> 455 <223> OTHER INFORMATION: Description of Artificial Sequence: adapter

INVALID Response

457 <400> SEQUENCE: 2-21
458 gatccccggg taccggggcc gcctcgcccg agctcgaatt cggccggcca tagcggccgc 60

461 <210> SEQ ID NO: 22
462 <211> LENGTH: 60

463 <212> TYPE: DNA

464 <213> ORGANISM: Artificial Sequence

466 <220> FEATURE:

E-> 467 <223> OTHER INFORMATION: Description of Artificial Sequence: adapter

469 <400> SEQUENCE: 3-22
470 aattgcggcc gctatggccg gccgaattcg agctcggcccg aggcggcctc ggtaccggg 60

473 <210> SEQ ID NO: 23
474 <211> LENGTH: 650

475 <212> TYPE: DNA

476 <213> ORGANISM: S.cerevisiae

E-> 478 <400> SEQUENCE: 4-23
See item # 11
on error Summary
Sheet.

RAW SEQUENCE LISTING

DATE: 02/07/2006

PATENT APPLICATION: US/10/522,366

TIME: 12:49:02

Input Set : A:\Sequence_Listing_10522366.txt

Output Set: N:\CRF4\02012006\J522366.raw

479 ggccgcctcg gccaggatct ggtggcgaac aagcatgcga tatttgcga cttaaaaagc 60
 480 tcaagtgc tc caaagaaaaa ccgaagtgcg ccaagtgtct gaagaacaac tggagtgtc 120
 481 gctactctcc caaaaaccaa aggtctccgc tgacttagggc acatctgaca gaagtggaat 180
 482 caaggctaga aagactggaa cagctatttc tactgatttt tcctcgagaa gaccttgaca 240
 483 tgattttgaa aatggattct ttacaggata taaaagcatt gttaacagga ttattttgtac 300
 484 aagataatgt gaataaaagat gccgtcacag atagattggc ttcagtggag actgataatgc 360
 485 ctctaacatt gagacagcat agaataagtg cgacatcatc atcggaaagag agtagtaaca 420
 486 aaggtaaag acagttgact gtatcgattt actcggcagc tcattatcatg aactccacaa 480
 487 ttccgttggaa ttttatgcc agggatgctc ttcatggatt tgattttgtct gaagaggatg 540
 488 acatgtcgga tggcttgccc ttccctgaaaa cggaccccaa caataatggg ttctttggcg 600
 489 acggttctct cttatgtatt ctctcgctgac tgactgaggc catagcggcc 650

492 <210> SEQ ID NO: 24

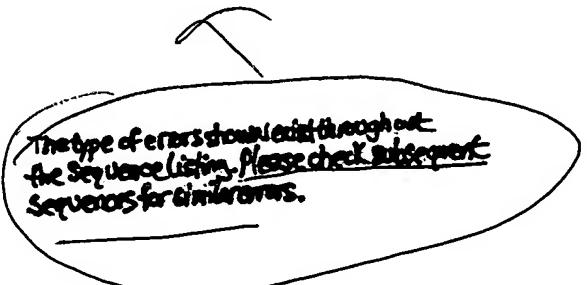
493 <211> LENGTH: 535

494 <212> TYPE: DNA

495 <213> ORGANISM: A. oryzae

E-> 497 <400> SEQUENCE: 5-24

498 ggccgcctcg gccattacta gtctactagt aactctgtct tatcgtcatc tcccataggt 60
 499 gagtttggtt gttttgttcc cactgagatc atgacctcct cctacccac catccacta 120
 500 tttttgttac ggttagccatg acccctccat ggcaaagaga gaggaggacg aggacgatca 180
 501 ggaaactgtg tctcgccgtc ataccacaat cgtgttatcc tgattgacat cttcttaat 240
 502 atcgttgtaa ctgttccctga ctctcggtca actgaaattt gatctccccca ccactgcctc 300
 503 taccttgtac tccgtgactg aaccatccga tcattcttt tgggtcgctcg gtgaacacaa 360
 504 ccccccgtgc tagtctcctt ccaacaccga tccagaattt ttttgatttt ccattccctt 420
 505 cgtttatatac tgcgtctct cctcccttcc cgtctttt cttccgtctt ccaagtttagt 480
 506 cgactgacca attccgcagc tcgtaaaaat gcctatcacc aaggccatag cggcc 535



The type of errors should exist throughout the Sequence listing. Please check subsequent Sequences for similar errors.

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/522,366

DATE: 02/07/2006

TIME: 12:49:03

Input Set : A:\Sequence_Listing_10522366.txt

Output Set: N:\CRF4\02012006\J522366.raw

3 M:270 C: Current Application Number differs, Replaced Application Number
10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
140 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:20 differs:1
157 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:21 differs:2
169 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:22 differs:3
178 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:23 differs:4
197 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:24 differs:5

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